

Amendments to the Drawings:

Please add the following new drawings, Figures 11, 12, 13, 14, 15, 16, 17, 18 and 19, after Figure 10. The attached new sheets of drawings includes Figures 11, 12, 13, 14, 15, 16, 17, 18 and 19 to be added.

Attachment: New Sheets

(3) Sequence Description: Figure 11

1 ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGCCCTGTGCAACCC  
5 MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro 16

49 ACTCGACTTCTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTG  
ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu 32

10 97 TATGAGCGCGATGAAGGTGATAAATGGCGAACAAAAAGTTGAATTG  
TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu 48

15 145 GGTTGGAGTTCCAATCTCCTATTATATTGATGGTATGTTAAA  
GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys 64

193 TTAACACAGTCTATGCCATCACGTTATAGCTGACAAGCACAAAC  
LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn 80

20 241 ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTCAATGCTTGAA  
MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu 96

289 GGAGCGGTTTGGATATTAGATAACGGTGTTCGAGAATTGCATATAGT  
GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer 112

25 337 AAAGACTTTGAAACTCTCAAAGTTGATTTCTTAGCAAGCTACCTGAA  
LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu 128

30 385 ATGCTGAAAATGTCGAAGATCGTTATGTCATAAACATATTAAAT  
MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn 144

433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTGAT  
GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp 160

35 481 GTGTTTATACATGGACCCAATGTGCCTGGATGCGTCCAAAATTA  
ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu 176

529    GTTTGTTTAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC  
 ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr   192

5      577    TTGAAATCCAGCAAGTATATAGCATGGCCTTGCAGGGCTGGCAAGCC  
 LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla   208

10     625    ACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCGCGT  
 ThrPheGlyGlyGlyAspHisProProLysSerAspLeuValProArg   224

15     673    GGATCCATGAGCACGATTCCAAACCTCAAAGAAAACCAAACGTAAC  
 GlySerMetSerThrIleProLysProGlnArgLysThrLysArgAsn   240

20     721    ACCAACCGTCGCCACAGGAATTACATCGTACTGACTGA  
 ThrAsnArgArgProGlnGluPheIleValThrAspEnd   252

25     (4)    Sequence Description: Figure 12

1      1 ATGTCCCCCTATACTAGGTTATTGGAAAATTAAAGGGCCTGTGCAACCC  
 MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro   16

20     49    ACTCGACTTCTTGAAATATCTTGAAGAAAAATATGAAGAGCATTG  
 ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu   32

25     97    TATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTGAATTG  
 TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu   48

30     145    GGTTTGGAGTTCCCAATCTCCTTATTATATTGATGGTGATGTTAAA  
 GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys   64

35     193    TTAACACAGTCTATGCCATACGTTATATAGCTGACAAGCACAAC  
 LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn   80

40     241    ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTCAATGCTTGAA  
 MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu   96

45     289    GGAGCGGTTTGGATATTAGATAACGGTGTTCGAGAATTGCATATAGT  
 GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer   112

337 AAAGACTTTGAAACTCTCAAAGTTGATTTCTTAGCAAGCTACCTGAA  
LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu 128

5 385 ATGCTGAAAATGTTCGAACGATCGTTATGTCATAAACATATTAAAT  
MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn 144

433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTTTGAT  
GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp 160

10 481 GTTGTAAACATGGACCCAATGTGCCTGGATGCGTTCCAAAATTAA  
ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu 176

529 GTTGTTTAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC  
15 ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr 192

577 TTGAAATCCAGCAAGTATATAGCATGGCCTTGCAAGGGCTGGCAAGCC  
LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla 208

20 625 ACGTTGGTGGTGGCGACCATCCTCCAAATCGGATCTGGTTCCGCGT  
ThrPheGlyGlyAspHisProProLysSerAspLeuValProArg 224

673 GGATCCGACGTCAAGTTCCCGGGTGGCGGTCAAGATCGTTGGTGGAGTT  
25 GlySerAspValLysPheProGlyGlyGlnIleValGlyGlyVal 240

721 TACTTGTGCCGCGCAGGGAATTCATCGTGACTGACTGA  
TyrLeuLeuProArgArgGluPheIleValThrAspEnd 252

5

(6) Sequence Description: Figure 13

1	ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro	16
10	49 ACTCGACTTCTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTG ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu	32
15	97 TATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTGAATTG TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu	48
20	145 GGTGGAGTTCCCAATCTCCTTATTATATTGATGGTGATGTTAAA GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys	64
25	193 TTAACACAGTCTATGCCATCATACGTTATATAGCTGACAAGCACAAAC LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn	80
30	241 ATGTTGGGTGGTGTCCAAAAGAGCGTCAGAGATTCAATGCTTGAA MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu	96
35	289 GGAGCGGTTTGGATATTAGATAACGGTGTTCGAGAATTGCATATAGT GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer	112
40	337 AAAGACTTGAAACTCTCAAAGTTGATTTCTAGCAAGCTACCTGAA LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu	128
45	385 ATGCTGAAAATGTCGAAGATCGTTATGTCATAAACATATTTAAAT MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn	144
50	433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTGAT GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp	160

481	GTGTTTATACATGGACCAATGTGCCTGGATGCGTCCAAAATTA ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu	176
5	529 GTTTGTTTAAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr	192
10	577 TTGAAATCCAGCAAGTATATAGCATGGCCTTGCAGGGCTGGCAAGCC LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla	208
15	625 ACGTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCGCGT ThrPheGlyGlyAspHisProProLysSerAspLeuValProArg	224
20	673 GGATCCAGCACGATTCCCAAACCTCAAAGAAAAACCAAACGTAACACC GlySerSerThrIleProLysProGlnArgLysThrLysArgAsnThr	240
	721 AACCGTCGCCACAGGACGTCAAGTTCCCGGGTGGCGGTCAAGATCGTT AsnArgArgProGlnAspValLysPheProGlyGlyGlnIleVal	256
	769 GGTGGAGTTACTTGTTGCCGCGCAGGAATTCACTCGTACTGACTGA GlyGlyValTyrLeuLeuProArgArgGluPheIleValThrAspEnd	271

(7) Sequence Description: Figure 14

5'-GATCCATGAGCACGATTCCCAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGC  
CCACAGG-3'

(8) Sequence Description: Figure 15

5'-AATTCCCTGTGGCGACGGTTGGTGTACGTTGGTTTCTTGAGGTTGGAAATCGT  
GCTCATG-3'

(9) Sequence Description: Figure 16

5'-GATCCGACGTCAAGTTCCCGGGTGGCGGTCAAGATCGTGGTGGAGTTACTTGTTGCCG  
CGCAGGG-3'

(10) Sequence Description: Figure 17

5'-AATTCCCTGCGCGAACAAAGTAAACTCCACCAACGATCTGACCGCCACCCGGGAACCT  
GACGTCG-3'

(13) Sequence Description: Figure 18

5'-GAATTCTTACCTGCGCGGCAACAAGTAAACTC-3'

(14) Sequence Description: Figure 19

5'-GCTGGATCCAGCACGATTCCAAACCTCAAAG-3'